

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: O'Brien, John S.
Kishimoto, Yasuo

(ii) TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson and Bear
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(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/484,594
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/100,247
(B) FILING DATE: 30-JUL-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Israelsen, Ned A
(B) REGISTRATION NUMBER: 29,655
(C) REFERENCE/DOCKET NUMBER: MYELOS.002DV2

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys	Glu	Phe	Leu	Val	Lys	Glu	Val	Thr	Lys	Leu	Ile	Asp	Asn	Asn	Lys
1				5					10					15	
Thr	Glu	Lys	Glu	Ile	Leu										
				20											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Tyr	Ala	Leu	Phe	Leu	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Ala	Leu	Ala
1				5					10					15	
Gly	Pro	Val	Leu	Gly	Leu	Lys	Glu	Cys	Thr	Arg	Gly	Ser	Ala	Val	Trp
			20					25					30		
Cys	Gln	Asn	Val	Lys	Thr	Ala	Ser	Asp	Cys	Gly	Ala	Val	Lys	His	Cys
		35					40					45			
Leu	Gln	Thr	Val	Trp	Asn	Lys	Pro	Thr	Val	Lys	Ser	Leu	Pro	Cys	Asp
	50					55					60				
Ile	Cys	Lys	Asp	Val	Val	Thr	Ala	Ala	Gly	Asp	Met	Leu	Lys	Asp	Asn
65					70					75					80
Ala	Thr	Glu	Glu	Glu	Ile	Leu	Val	Tyr	Leu	Glu	Lys	Thr	Cys	Asp	Trp
				85					90					95	
Leu	Pro	Lys	Pro	Asn	Met	Ser	Ala	Ser	Cys	Lys	Glu	Ile	Val	Asp	Ser
			100					105					110		
Tyr	Leu	Pro	Val	Ile	Leu	Asp	Ile	Ile	Lys	Gly	Glu	Met	Ser	Arg	Pro
		115					120					125			
Gly	Glu	Val	Cys	Ser	Ala	Leu	Asn	Leu	Cys	Glu	Ser	Leu	Gln	Lys	His
	130					135					140				
Leu	Ala	Glu	Leu	Asn	His	Gln	Lys	Gln	Leu	Glu	Ser	Asn	Lys	Ile	Pro
145					150					155					160
Glu	Leu	Asp	Met	Thr	Glu	Val	Val	Ala	Pro	Phe	Met	Ala	Asn	Ile	Pro
				165					170					175	
Leu	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Arg	Ser	Lys	Pro	Gln	Pro	Lys
			180					185					190		
Asp	Gly	Asp	Val	Cys	Gln	Asp	Cys	Ile	Gln	Met	Val	Thr	Asp	Ile	Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Asp	Val	Tyr	Cys	Glu	Val	Cys	Glu	Phe	Leu	Val	Lys	Glu	Val	Thr
1				5					10					15	
Lys	Leu	Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu	Ile	Leu	Asp	Ala	Phe
			20					25					30		
Asp	Lys	Met	Cys	Ser	Lys	Leu	Pro	Lys	Ser	Leu	Ser	Glu	Glu	Cys	Gln
		35					40					45			
Glu	Val	Val	Asp	Thr	Tyr	Gly	Ser	Ser	Ile	Leu	Ser	Ile	Leu	Leu	Glu
	50					55					60				
Glu	Val	Ser	Pro	Glu	Leu	Val	Cys	Ser	Met	Leu	His	Leu	Cys	Ser	Gly
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTACGCCC	TCTTCCTCCT	GGCCAGCCTC	CTGGGCGCGG	CTCTAGCCGG	CCCGGTCCTT	60
GGACTGAAAG	AATGCACCAG	GGGCTCGGCA	GTGTGGTGCC	AGAATGTGAA	GACGGCGTCC	120
GACTGCGGGG	CAGTGAAGCA	CTGCCTGCAG	ACCGTTTGGA	ACAAGCCAAC	AGTGAAATCC	180
CTTCCCTGCG	ACATATGCAA	AGACGTTGTC	ACCGCAGCTG	GTGATATGCT	GAAGGACAAT	240
GCCACTGAGG	AGGAGATCCT	TGTTTACTTG	GAGAAGACCT	GTGACTGGCT	TCCGAAACCG	300
AACATGTCTG	CTTCATGCAA	GGAGATAGTG	GACTCCTACC	TCCCTGTCAT	CCTGGACATC	360
ATTAAAGGAG	AAATGAGCCG	TCCTGGGGAG	GTGTGCTCTG	CTCTCAACCT	CTGCGAGTCT	420
CTCCAGAAGC	ACCTAGCAGA	GCTGAATCAC	CAGAAGCAGC	TGGAGTCCAA	TAAGATCCCA	480
GAGCTGGACA	TGACTGAGGT	GGTGGCCCCC	TTCATGGCCA	ACATCCCTCT	CCTCCTCTAC	540
CCTCAGGACG	GCCCCCGCAG	CAAGCCCCAG	CCAAAGGATA	ATGGGGACGT	TTGCCAGGAC	600
TGCATTGAGA	TGGTGACTGA	CATCCAGACT	GCTGTACGGA	CCAACCTCCAC	CTTTGTCCAG	660
GCCTTGGTGG	AACATGTCAA	GGAGGAGTGT	GACCGCCTGG	GCCCTGGCAT	GGCCGACATA	720
TGCAAGAAGT	ATATCAGCCA	GTATTCTGAA	ATTGCTATCC	AGATGATGAT	GCACATGCAA	780
CCCAAGGAGA	TCTGTGCGCT	GGTTGGGTTC	TGTGATGAGG	TGAAAGAGAT	GCCCATGCAG	840
ACTCTGGTCC	CCGCCAAAGT	GGCCTCCAAG	AATGTCATCC	CTGCCCTGGA	ACTGGTGGAG	900
CCCATTAAAG	AGCACGAGGT	CCCAGCAAAG	TCTGATGTTT	ACTGTGAGGT	GTGTGAATTC	960
CTGGTGAAGG	AGGTGACCAA	GCTGATTGAC	AACAACAAGA	CTGAGAAAGA	AATACTCGAC	1020
GCTTTTGACA	AAATGTGCTC	GAAGCTGCCG	AAGTCCCTGT	CGGAAGAGTG	CCAGGAGGTG	1080
GTGGACACGT	ACGGCAGCTC	CATCCTGTCC	ATCCTGCTGG	AGGAGGTCAG	CCCTGAGCTG	1140
GTGTGCAGCA	TGCTGCACCT	CTGCTCTGGC	ACGCGGCTGC	CTGCACTGAC	CGTTCACGTG	1200
ACTCAGCCAA	AGGACGGTGG	CTTCTGCGAA	GTGTGCAAGA	AGCTGGTGGG	TTATTTGGAT	1260
CGCAACCTGG	AGAAAAACAG	CACCAAGCAG	GAGATCCTGG	CTGCTCTTGA	GAAAGGCTGC	1320
AGCTTCCTGC	CAGACCCCTTA	CCAGAAGCAG	TGTGATCAGT	TTGTGGCAGA	GTACGAGCCC	1380
GTGCTGATCG	AGATCCTGGT	GGAGGTGATG	GATCCTTCCT	TCGTGTGCTT	GAAAATTGGA	1440
GCCTGCCCTT	CGGCCCATAA	GCCCTTGTTG	GGAAGTGAAG	AGTGTATATG	GGGCCCAAGC	1500
TACTGGTGCC	AGAACACAGA	GACAGCAGCC	CAGTGCAATG	CTGTGAGGCA	TTGCAAACGC	1560
CATGTGTGGA	ACTAGGAGGA	GGAATATTCC	ATCTTGGCAG	AAACCACAGC	ATTGGTTTTT	1620

TTCTACTTGT	GTGTCTGGGG	GAATGAACGC	ACAGATCTGT	TTGACTTTGT	TATAAAAATA	1680
GGGCTCCCCC	ACCTCCCCCA	TTTCTGTGTC	CTTTATTGTA	GCATTGCTGT	CTGCAAGGGA	1740
GGCCCTAGCC	CCTGGCAGAC	ATAGCTGCTT	CAGTGCCCCT	TTTCTCTCTG	CTAGATGGAT	1800
GTTGATGCAC	TGGAGGTCTT	TTAGCCTGCC	CTTGCATGGC	GCCTGCTGGA	GGAGGAGAGA	1860
GCTCTGCTGG	CATGAGCCAC	AGTTTCTTGA	CTGGAGGCCA	TCAACCCTCT	TGGTTGAGGC	1920
CTTGTTCTGA	GCCCTGACAT	GTGCTTGGGC	ACTGGTGGGC	CTGGGCTTCT	GAGGTGGCCT	1980
CCTGCCCTGA	TCAGGGACCC	TCCCCGCTTT	CCTGGGCCTC	TCAGTTGAAC	AAAGCAGCAA	2040
AACAAAGGCA	GTTTTATATG	AAAGATTAGA	AGCCTGGAAT	AATCAGGCTT	TTTAAATGAT	2100
GTAATTCCCA	CTGTAATAGC	ATAGGGATTT	TGGAAGCAGC	TGCTGGTGGC	TTGGGACATC	2160
AGTGGGGCCA	AGGGTTCTCT	GTCCCTGGTT	CAACTGTGAT	TTGGCTTTCC	CGTGTCTTTC	2220
CTGGTGATGC	CTTGTTTGGG	GTTCTGTGGG	TTTGGGTGGG	AAGAGGGCAA	TCTGCCTGAA	2280
TGTAACCTGC	TAGCTCTCCG	AAGGCCCTGC	GGGCCTGGCT	TGTGTGAGCG	TGTGGACAGT	2340
GGTGGCCGCG	CTGTGCCTGC	TCGTGTTGCC	TACATGTCCC	TGGCTGTTGA	GGCGCTGCTT	2400
CAGCCTGCAC	CCCTCCCTTG	TCTCATAGAT	GCTCCTTTTG	ACCTTTTCAA	ATAAATATGG	2460
ATGGCGAGCT	CCTAGGCCTC	TGGCTTCCTG	GTAGAGGGCG	GCATGCCGAA	GGGTCTGCTG	2520
GGTGTGGATT	GGATGCTGGG	GTGTGGGGGT	TGGAAGCTGT	CTGTGGCCCA	CTTGGGCACC	2580
CACGCTTCTG	TCCACTTCTG	GTTGCCAGGA	GACAGCAAGC	AAAGCCAGCA	GGACATGAAG	2640
TTGCTATTAA	ATGGACTTCG	TGATTTTGTG	TTTGCATAAA	AGTTTCTGTG	ATTTAACAAT	2700
AAAATTCTGT	TAGCCAGAAA	AAAAAAAAAA	AAAAAAAAAA			2740

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Lys	Glu	Val	Thr	Lys	Leu	Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu
1				5				10					15		
Ile	Leu														

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Gln	Phe	Val	Met	Asn	Lys	Phe	Ser	Glu	Leu	Ile	Val	Asn	Asn	Ala
1				5				10					15		

Thr Glu Glu Leu Leu Tyr
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Gln Leu Val Asn Arg Lys Leu Ser Glu Leu Ile Ile Asn Asn Ala
1 5 10 15
Thr Glu Glu Leu Leu
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Glu Tyr Val Val Lys Lys Val Met Leu Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Lys Ile Ile
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Glu Phe Val Val Lys Glu Val Ala Lys Leu Ile Asp Asn Asn Arg
1 5 10 15
Thr Glu Glu Glu Ile Leu

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 21...21
- (D) OTHER INFORMATION: Xaa=I or L

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Leu Ile Xaa Asn Asn Xaa
 1 5 10 15
 Thr Glu Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn Ala
 1 5 10 15
 Thr Glu Glu Glu Ile Leu
 20